



Rec'd PCT/TT3

16 APR 2001

## SEQUENCE LISTING

<110> Sim, Gek-Kee  
Dreitz, Matthew J.

<120> T CELL RECEPTOR PROTEINS, NUCLEIC ACID MOLECULES, AND  
USES THEREOF

<130> IM-3-C1-PCT

<140> not yet assigned

<141> 1999-07-29

<150> 60/094,506

<151> 1998-07-29

<160> 100

<170> WordPerfect for Windows 8.0

<210> 1

<211> 381

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(381)

<400> 1

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1				5					10					15		
ttg	aac	gca	caa	gtg	act	caa	acc	ccg	aga	caa	ctc	atc	aaa	aaa	gtg	96
Leu	Asn	Ala	Gln	Val	Thr	Gln	Thr	Pro	Arg	Gln	Leu	Ile	Lys	Lys	Val	
			20					25					30			
gga	gcg	aaa	gtt	ttg	ttg	aaa	tgt	tca	cag	aat	atg	gac	cat	gaa	aga	144
Gly	Ala	Lys	Val	Leu	Leu	Lys	Cys	Ser	Gln	Asn	Met	Asp	His	Glu	Arg	
		35					40					45				
atg	ttc	tgg	tat	cga	caa	gac	cca	ggt	ctg	ggg	ttg	cgg	ctg	ctc	tac	192
Met	Phe	Trp	Tyr	Arg	Gln	Asp	Pro	Gly	Leu	Gly	Leu	Arg	Leu	Leu	Tyr	
	50					55					60					
tgg	tcc	tat	aat	att	gac	agt	gtt	gag	aca	gga	gac	atc	cct	tat	ggg	240
Trp	Ser	Tyr	Asn	Ile	Asp	Ser	Val	Glu	Thr	Gly	Asp	Ile	Pro	Tyr	Gly	
	65				70					75				80		
tac	agt	gtc	tcg	agg	aag	aag	aag	gat	gcc	ttc	ccc	ttg	att	ctg	gag	288
Tyr	Ser	Val	Ser	Arg	Lys	Lys	Lys	Asp	Ala	Phe	Pro	Leu	Ile	Leu	Glu	
				85				90						95		
tct	gct	cgc	atc	aac	cag	aca	tct	gtg	tac	ttc	tgc	gcc	agc	agc	ccg	336
Ser	Ala	Arg	Ile	Asn	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser	Ser	Pro	

100	105	110	
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115	120	125	

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 <213> Canis familiaris

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Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val  
 20 25 30

Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg  
 35 40 45

Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr  
 50 55 60

Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly  
 65 70 75 80

Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu  
 85 90 95

Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Pro  
 100 105 110

Phe Ser Gln Asn Thr Gln Tyr Phe Gly Ala Gly Thr Arg Leu Leu  
 115 120 125

<210> 3  
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 cttcttcttc gagacactgt acccataagg gatgtctcct gtctcaacac tgtcaatatt 180  
 ataggaccag tagagcagcc gcaaccccag acctgggtct tgcgataacc agaacattct 240  
 ttcattgggtcc atattctgtg aacatttcaa caaaactttc gctcccactt ttttgatgag 300  
 ttgtctcggg gtttgagtca cttgtgcgtt caaaaggcct actcccagga aacaaaaggc 360  
 cacaccacag aggagtccga t 381



Ala	Leu	Val	Ser	Gln	Lys	Pro	Arg	Arg	Asp	Ile	Cys	Gln	Arg	Gly	Thr
			20					25				30			
Ser	Ile	Thr	Ile	His	Cys	Glu	Val	Asp	Thr	Gln	Val	Thr	Leu	Met	Phe
		35					40				45				
Trp	Tyr	Arg	Gln	Leu	Pro	Gly	Gln	Ser	Leu	Ile	Leu	Ile	Ala	Thr	Ala
	50					55					60				
Asn	Gln	Gly	Ala	Glu	Ala	Thr	Tyr	Glu	Ser	Gly	Phe	Thr	Arg	Glu	Lys
	65				70					75				80	
Phe	Pro	Ile	Ser	Arg	Arg	Thr	Leu	Met	Phe	Ser	Thr	Leu	Thr	Val	Ser
				85					90					95	
Asn	Leu	Ser	Leu	Glu	Asp	Thr	Ser	Ser	Tyr	Phe	Cys	Ser	Ile	Trp	Tyr
			100				105						110		
Gly	Glu	Gly	Glu	Gln	His	Phe	Gly	Pro	Gly	Thr	Arg	Leu	Thr	Val	Leu
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 <213> Canis familiaris

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 tagggttcgg cggtgatgg gaaacttctc cctggtaa at ccactttcgt aggtggcctc 180  
 tgcaccctgg tttgcggttg caatcagtat caagctctgt cctgggagct gacggtagca 240  
 gaacatcaag gtgacttggg tatcgacctc acagtggatg gtaatggagg tcccacgttg 300  
 acagatgtcc ctgcgcggct tttgagagac aagagctcca aacacagagc cttgtcccag 360  
 gaggagtagc aggcaagtca gcatctttag gtgctagccc ttcaccgt 408

<210> 7  
 <211> 384  
 <212> DNA  
 <213> Canis familiaris

<400> 7  
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 Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly  
 1 5 10 15  
 gct ctt gtc tct caa aag ccg cgc agg gac atc tgt caa cgt ggg acc 96  
 Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr  
 20 25 30

tcc att acc atc cac tgt gag gtc gat acc caa gtc acc ttg atg ttc	144
Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe	
35 40 45	

tgg tac cgt cag ctc cca gga cag agc ttg ata ctg att gca acc gca	192
Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala	
50 55 60	

aac cag ggt gca gag gcc acc tac gaa agt gga ttt acc agg gag aag	240
Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys	
65 70 75 80	

ttt ccc atc agc cgc cga acc cta atg ttc tcc act ctg act gtg agc	288
Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser	
85 90 95	

aac ctg agc ctc gaa gac acc agc tct tac ttc tgc agc att tgg tac	336
Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser Ile Trp Tyr	
100 105 110	

ggg gag ggg gag cag cac ttt ggg cca ggg acc cgg ctc acc gtc cta	384
Gly Glu Gly Glu Gln His Phe Gly Pro Gly Thr Arg Leu Thr Val Leu	
115 120 125	

<210> 8

<211> 384

<212> DNA

<213> Canis familiaris

<400> 8

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gcagaagtaa gagctggtgt cttcgaggct cagggttgtc acagtcagag tggagaacat	120
tagggttcgg cggtgatgg gaaacttctc cctggtaaatt ccactttcgt aggtggcctc	180
tgcaccctgg tttgcggttg caatcagtat caagctctgt cctgggagct gacgggtacca	240
gaacatcaag gtgacttggg tatcgacctc acagtggatg gtaatggagg tcccacgttg	300
acagatgtcc ctgcgcggct tttgagagac aagagctcca aacacagagc cttgtcccag	360
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<210> 9

<211> 408

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (7)..(408)

<400> 9

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tgg aca gga tac atg gat gct gga att atc cag agc cca aga tac aag	96
Trp Thr Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys	
15 20 25 30	
gtc aca ggg aca gga aag agg gtg act ctg aga tgt cac cag aca gac	144
Val Thr Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp	
35 40 45	
aac tat gac tat atg tac tgg tat cga cat gac ctg gga cat ggg ccg	192
Asn Tyr Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro	
50 55 60	
agg ctg atc tat tat tca aat ggt att aac agc act gaa aaa gga gac	240
Arg Leu Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp	
65 70 75	
ctc tcc aat gga tac aca gtc tct aga tca aac aag atg gat ttc ccc	288
Leu Ser Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro	
80 85 90	
ctc cta ctg gac tct gtt acc tcc tcc cag aca tct gtg tac ttc tgt	336
Leu Leu Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys	
95 100 105 110	
gcc gac acg agg gat cct gtt gca gta aat tat gat ttt aac ttt ggc	384
Ala Asp Thr Arg Asp Pro Val Ala Val Asn Tyr Asp Phe Asn Phe Gly	
115 120 125	
cca ggg acc aag ctg aca gtc gta	408
Pro Gly Thr Lys Leu Thr Val Val	
130	

<210> 10  
 <211> 134  
 <212> PRT  
 <213> Canis familiaris

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Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr	
35 40 45	
Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu	
50 55 60	
Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser	
65 70 75 80	
Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu	
85 90 95	

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala Asp  
 100 105 110

Thr Arg Asp Pro Val Ala Val Asn Tyr Asp Phe Asn Phe Gly Pro Gly  
 115 120 125

Thr Lys Leu Thr Val Val  
 130

<210> 11  
 <211> 408  
 <212> DNA  
 <213> Canis familiaris

<400> 11  
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 ggggaaatcc atcttggttg atctagagac tgtgtatcca ttggagaggt ctcttttttc 180  
 agtgctgtta ataccatttg aataatagat cagcctcggc ccatgtccca ggtcatgtcg 240  
 ataccagtac atatagtcac agttgtctgt ctgggtgacat ctcagagtca ccctctttcc 300  
 tgtccctgtg accttgatc ttgggctctg gataattcca gcatccatgt atcctgtcca 360  
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<210> 12  
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 <213> Canis familiaris

<220>  
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 <222> (1)..(402)

<400> 12  
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 Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr  
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 gga tac atg gat gct gga att atc cag agc cca aga tac aag gtc aca 96  
 Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr  
 20 25 30  
 ggg aca gga aag agg gtg act ctg aga tgt cac cag aca gac aac tat 144  
 Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr  
 35 40 45  
 gac tat atg tac tgg tat cga cat gac ctg gga cat ggg ccg agg ctg 192  
 Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu

50	55	60	
atc tat tat tca aat ggt att aac agc act gaa aaa gga gac ctc tcc			240
Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser			
65	70	75	80
aat gga tac aca gtc tct aga tca aac aag atg gat ttc ccc ctc cta			288
Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu			
	85	90	95
ctg gac tct gtt acc tcc tcc cag aca tct gtg tac ttc tgt gcc gac			336
Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala Asp			
	100	105	110
acg agg gat cct gtt gca gta aat tat gat ttt aac ttt ggc cca ggg			384
Thr Arg Asp Pro Val Ala Val Asn Tyr Asp Phe Asn Phe Gly Pro Gly			
	115	120	125
acc aag ctg aca gtc gta			402
Thr Lys Leu Thr Val Val			
130			

<210> 13  
 <211> 402  
 <212> DNA  
 <213> Canis familiaris

<400> 13  
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 ggggaaatcc atcttgtttg atctagagac tgtgtatcca ttggagaggt ctccctttttc 180  
 agtgctgtta ataccatttg aataatagat cagcctcggc ccatgtccca ggcatgtcg 240  
 ataccagtac atatagtcac agttgtctgt ctggtgacat ctcagagtca ccctctttcc 300  
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 caggacacaa agagccatgc caaagaagac gccgggtggcc at 402

<210> 14  
 <211> 483  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (85)..(483)

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ggctatcagc ttcccagggc tgcc atg ggc tcc agg ctt ctc tgc tgt gtg 111  
Met Gly Ser Arg Leu Leu Cys Cys Val  
1 5

gcc ctt tgt ctc ctg gga gcc ggc ccc gtg gag tct gag gtc atc caa 159  
Ala Leu Cys Leu Leu Gly Ala Gly Pro Val Glu Ser Glu Val Ile Gln  
10 15 20 25

act cca aga cac atg atc aaa gca aga gga cag aca gtg acc ctg aga 207  
Thr Pro Arg His Met Ile Lys Ala Arg Gly Gln Thr Val Thr Leu Arg  
30 35 40

tgt tcc ctt atc tct gga cac cta tct gtg tac tgg tac caa cag gcc 255  
Cys Ser Leu Ile Ser Gly His Leu Ser Val Tyr Trp Tyr Gln Gln Ala  
45 50 55

ctg ggc cag ggt ccc cgg ttt ctc att cag tat tac aat agg gaa gag 303  
Leu Gly Gln Gly Pro Arg Phe Leu Ile Gln Tyr Tyr Asn Arg Glu Glu  
60 65 70

aga gac aaa gga gac atc ccg gca aga ttc tca gtg cag cag ttc agt 351  
Arg Asp Lys Gly Asp Ile Pro Ala Arg Phe Ser Val Gln Gln Phe Ser  
75 80 85

aac tac agc tcc cag ctg gag atg aac tcc ctg gag cca gga gac tca 399  
Asn Tyr Ser Ser Gln Leu Glu Met Asn Ser Leu Glu Pro Gly Asp Ser  
90 95 100 105

gcc cta tat ctc tgt gcc agc agc tta gat gcg ttc gac gcg ggg cag 447  
Ala Leu Tyr Leu Cys Ala Ser Ser Leu Asp Ala Phe Asp Ala Gly Gln  
110 115 120

ctg tac ttc ggg gcc ggt tcc aag ctg gcc gtg ctg 483  
Leu Tyr Phe Gly Ala Gly Ser Lys Leu Ala Val Leu  
125 130

<210> 15

<211> 133

<212> PRT

<213> Canis familiaris

<400> 15

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala  
1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys  
20 25 30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His  
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe  
50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro

65		70		75		80									
Ala	Arg	Phe	Ser	Val	Gln	Gln	Phe	Ser	Asn	Tyr	Ser	Ser	Gln	Leu	Glu
				85					90					95	
Met	Asn	Ser	Leu	Glu	Pro	Gly	Asp	Ser	Ala	Leu	Tyr	Leu	Cys	Ala	Ser
			100					105					110		
Ser	Leu	Asp	Ala	Phe	Asp	Ala	Gly	Gln	Leu	Tyr	Phe	Gly	Ala	Gly	Ser
		115					120					125			
Lys	Leu	Ala	Val	Leu											
	130														

<210> 16  
 <211> 483  
 <212> DNA  
 <213> Canis familiaris

<400> 16  
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 ggagctgtag ttactgaact gctgcactga gaatcttgcc gggatgtctc ctttgtctct 180  
 ctcttcctta ttgtaatact gaatgagaaa ccgggggaccc tggcccaggc cctgttggtta 240  
 ccagtaacaca gataggtgtc cagagataag ggaacatctc agggtcactg tctgtcctct 300  
 tgctttgatc atgtgtcttg gagtttgat gacctcagac tccacggggc cggtccccag 360  
 gagacaaagg gccacacagc agagaagcct ggagcccatg gcagccctgg gaagctgata 420  
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<210> 17  
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 <212> DNA  
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<220>  
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 <222> (1)..(399)

<400> 17  
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 1 5 10 15  
 ggc ccc gtg gag tct gag gtc atc caa act cca aga cac atg atc aaa 96  
 Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys  
 20 25 30

gca aga gga cag aca gtg acc ctg aga tgt tcc ctt atc tct gga cac	144
Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His	
35 40 45	
cta tct gtg tac tgg tac caa cag gcc ctg ggc cag ggt ccc cgg ttt	192
Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe	
50 55 60	
ctc att cag tat tac aat agg gaa gag aga gac aaa gga gac atc ccg	240
Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro	
65 70 75 80	
gca aga ttc tca gtg cag cag ttc agt aac tac agc tcc cag ctg gag	288
Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu	
85 90 95	
atg aac tcc ctg gag cca gga gac tca gcc cta tat ctc tgt gcc agc	336
Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser	
100 105 110	
agc tta gat gcg ttc gac gcg ggg cag ctg tac ttc ggg gcc ggt tcc	384
Ser Leu Asp Ala Phe Asp Ala Gly Gln Leu Tyr Phe Gly Ala Gly Ser	
115 120 125	
aag ctg gcc gtg ctg	399
Lys Leu Ala Val Leu	
130	

<210> 18  
 <211> 399  
 <212> DNA  
 <213> Canis familiaris

<400> 18  
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 ggagctgtag ttactgaact gctgcactga gaatcttgcc gggatgtctc ctttgtctct 180  
  
 ctcttcctta ttgtaatact gaatgagaaa cgggggaccc tggcccaggg cctgttggtta 240  
  
 ccagtacaca gataggtgtc cagagataag ggaacatctc agggtcactg tctgtcctct 300  
  
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 gagacaaagg gccacacagc agagaagcct ggagcccat 399

<210> 19  
 <211> 462  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS

<222> (73)..(462)

<400> 19

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catcacctga ag atg ctg atg ctt ctg ctg ctc ctg ggg ccc agc tct gga 111  
Met Leu Met Leu Leu Leu Leu Leu Gly Pro Ser Ser Gly

1 5 10

ctc ggt gcc ctc gtc ttc cag gcg ccc agc aca atg atc tgt aag agc 159  
Leu Gly Ala Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser  
15 20 25

gga gcc acc gtg cag atc cag tgt caa aca gtg gac ctt caa gcc aca 207  
Gly Ala Thr Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr  
30 35 40 45

acc gtg ttt tgg tat cgc cag ctc ccg aag cag ggc ctt acc ctt atg 255  
Thr Val Phe Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met  
50 55 60

gtg acc tct aac gtg ggc aac agt gct aca cac gag cag ggg ttc cct 303  
Val Thr Ser Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro  
65 70 75

gca gcc aag ttc cct gtt aac cac cca aac ctc acg ttt tcc tcc ctg 351  
Ala Ala Lys Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu  
80 85 90

atg gtg acg agt tca ggt cct gga gac agc ggc ctc tac ttc tgt ggt 399  
Met Val Thr Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Gly  
95 100 105

gtt cgg gcg tat ggt ggg aac tcg ccc ctc tac ttt gga aca ggc acc 447  
Val Arg Ala Tyr Gly Gly Asn Ser Pro Leu Tyr Phe Gly Thr Gly Thr  
110 115 120 125

agg ctc acc gtg aca 462  
Arg Leu Thr Val Thr  
130

<210> 20

<211> 130

<212> PRT

<213> Canis familiaris

<400> 20

Met Leu Met Leu Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala  
1 5 10 15

Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr  
20 25 30

Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe  
35 40 45

Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser  
           50                          55                          60  
 Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys  
           65                          70                          75                          80  
 Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr  
                           85                          90                          95  
 Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Gly Val Arg Ala  
                           100                          105                          110  
 Tyr Gly Gly Asn Ser Pro Leu Tyr Phe Gly Thr Gly Thr Arg Leu Thr  
           115                          120                          125  
 Val Thr  
           130

<210> 21  
 <211> 462  
 <212> DNA  
 <213> Canis familiaris

<400> 21  
 tgtcacggtg agcctggtgc ctgttccaaa gtagaggggc gagttccac catacgcccg 60  
 aacaccacag aagtagaggc cgctgtctcc aggacctgaa ctcgtcacca tcagggagga 120  
 aaacgtgagg tttgggtggt taacagggaa cttggctgca gggaaccct gctcgtgtgt 180  
 agcactgttg cccacgtagg aggtcaccat aagggttaagg ccctgcttcg ggagctggcg 240  
 ataccaaaac acggttgtgg cttgaagggtc cactgtttga cactggatct gcacggtggc 300  
 tccgctctta cagatcattg tgctggggcg ctggaagacg agggcaccga gtccagagct 360  
 gggccccagg agcagcagaa gcatcagcat cttcaggtga tggcctcata ccatacctct 420  
 ctcaagatag atatgaccac gcctcgtgcc gaatcctgca gc 462

<210> 22  
 <211> 417  
 <212> DNA  
 <213> Canis familiaris  
 <220>  
 <221> CDS  
 <222> (13)..(417)

<400> 22  
 cacgagcctg cc atg tgc cca gtg ttc atc tgc tcc ttg gtc ctc tgg ctc 51  
                   Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu  
                   1                  5                  10  
 ctg agt aca ggc acc ctc aat gca aaa gtc atg cag act cca gga cat 99

Leu	Ser	Thr	Gly	Thr	Leu	Asn	Ala	Lys	Val	Met	Gln	Thr	Pro	Gly	His	
15						20					25					
ctg	gtc	aaa	ggg	aaa	gga	caa	aaa	gca	aaa	atg	gaa	tgt	gtc	cca	ata	147
Leu	Val	Lys	Gly	Lys	Gly	Gln	Lys	Ala	Lys	Met	Glu	Cys	Val	Pro	Ile	
30					35					40					45	
aaa	gga	cat	agt	tat	gtt	ttc	tgg	tat	cag	cag	atc	cca	gca	aaa	gag	195
Lys	Gly	His	Ser	Tyr	Val	Phe	Trp	Tyr	Gln	Gln	Ile	Pro	Ala	Lys	Glu	
				50					55					60		
ttc	aag	ttc	ttg	att	tct	ttc	cag	gat	aac	gct	gtc	ttt	gat	aaa	aca	243
Phe	Lys	Phe	Leu	Ile	Ser	Phe	Gln	Asp	Asn	Ala	Val	Phe	Asp	Lys	Thr	
			65					70					75			
ggg	atg	ccc	acg	cag	aga	ttt	tta	gcc	ttg	tgt	cca	aaa	aac	cta	ccc	291
Gly	Met	Pro	Thr	Gln	Arg	Phe	Leu	Ala	Leu	Cys	Pro	Lys	Asn	Leu	Pro	
		80					85					90				
tgt	agc	cta	gag	atc	gag	cgt	aca	gag	ctg	cag	gat	tca	gcc	gtg	tat	339
Cys	Ser	Leu	Glu	Ile	Glu	Arg	Thr	Glu	Leu	Gln	Asp	Ser	Ala	Val	Tyr	
	95					100					105					
ttt	tgt	gcc	agc	agt	gac	aga	act	ggg	gga	ctc	gtt	cac	gag	cag	tat	387
Phe	Cys	Ala	Ser	Ser	Asp	Arg	Thr	Gly	Gly	Leu	Val	His	Glu	Gln	Tyr	
110					115					120				125		
ttc	ggc	gcc	ggc	acc	agg	ctc	acg	gtc	ctc							417
Phe	Gly	Ala	Gly	Thr	Arg	Leu	Thr	Val	Leu							
				130					135							

<210> 23  
 <211> 135  
 <212> PRT  
 <213> Canis familiaris

Met	Cys	Pro	Val	Phe	Ile	Cys	Ser	Leu	Val	Leu	Trp	Leu	Leu	Ser	Thr	
1				5					10					15		
Gly	Thr	Leu	Asn	Ala	Lys	Val	Met	Gln	Thr	Pro	Gly	His	Leu	Val	Lys	
			20					25					30			
Gly	Lys	Gly	Gln	Lys	Ala	Lys	Met	Glu	Cys	Val	Pro	Ile	Lys	Gly	His	
		35					40					45				
Ser	Tyr	Val	Phe	Trp	Tyr	Gln	Gln	Ile	Pro	Ala	Lys	Glu	Phe	Lys	Phe	
	50					55					60					
Leu	Ile	Ser	Phe	Gln	Asp	Asn	Ala	Val	Phe	Asp	Lys	Thr	Gly	Met	Pro	
65					70					75					80	
Thr	Gln	Arg	Phe	Leu	Ala	Leu	Cys	Pro	Lys	Asn	Leu	Pro	Cys	Ser	Leu	
				85					90					95		

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Ala  
100 105 110

Ser Ser Asp Arg Thr Gly Gly Leu Val His Glu Gln Tyr Phe Gly Ala  
115 120 125

Gly Thr Arg Leu Thr Val Leu  
130 135

<210> 24  
<211> 417  
<212> DNA  
<213> Canis familiaris

<400> 24  
gaggaccgtg agcctgggtgc cggcgccgaa atactgctcg tgaacgagtc cccagttct 60  
gtcactgctg gcacaaaaat acacggctga atcctgcagc tctgtacgct cgatctctag 120  
gctacagggt aggttttttg gacacaaggc taaaaatctc tgcgtgggca tccctgtttt 180  
atcaaagaca gcgttatcct ggaaagaaat caagaacttg aactcttttg ctgggatctg 240  
ctgataccag aaaacataac tatgtccttt tattgggaca cattccattt ttgctttttg 300  
tcctttccct ttgaccagat gtcctggagt ctgcatgact tttgcattga gggcgctgt 360  
actcaggagc cagaggacca aggagcagat gaacactggg cacatggcag gctcgtg 417

<210> 25  
<211> 423  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (40)..(423)

<400> 25  
ggcagagca ctgaggacca gactgtgcct gtctccacc atg ggc tcc ggg ttc 54  
Met Gly Ser Gly Phe  
1 5

ctc tgc tgt atg gtc ctc tgc ctc ctg gga gca gca ccc ctg gac aca 102  
Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala Ala Pro Leu Asp Thr  
10 15 20

aca gtt tcc cag act cca aga tac ctc atc gcg cac gtg gga tcg aag 150  
Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala His Val Gly Ser Lys  
25 30 35

aag tta cta aaa tgt gag caa aat ctg ggc cat aat gct atg tac tgg 198  
Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His Asn Ala Met Tyr Trp  
40 45 50

tat aag caa gac ctc aag caa ctg ctg aag atc atg ttt atc tac ttt	246
Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile Met Phe Ile Tyr Phe	
55 60 65	

aat cag gga ctc aat cta aat gaa tca gtt cca ggt cgt ttc tca cct	294
Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro Gly Arg Phe Ser Pro	
70 75 80 85	

gag aca ctg aca agc tca tta act tca tgt cga ctc ctg aac agt gac	342
Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg Leu Leu Asn Ser Asp	
90 95 100	

tct gct gtg tat ttc tgt gcc agc agc gag ggg tat gat gaa aaa ttg	390
Ser Ala Val Tyr Phe Cys Ala Ser Ser Glu Gly Tyr Asp Glu Lys Leu	
105 110 115	

tat ttt gca agt gga acc aag ctt tct gtc ttg	423
Tyr Phe Ala Ser Gly Thr Lys Leu Ser Val Leu	
120 125	

<210> 26  
 <211> 128  
 <212> PRT  
 <213> Canis familiaris

<400> 26	
Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala	
1 5 10 15	

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala	
20 25 30	

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His	
35 40 45	

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile	
50 55 60	

Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro	
65 70 75 80	

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg	
85 90 95	

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser Glu Gly	
100 105 110	

Tyr Asp Glu Lys Leu Tyr Phe Ala Ser Gly Thr Lys Leu Ser Val Leu	
115 120 125	

<210> 27  
 <211> 423  
 <212> DNA  
 <213> Canis familiaris



<400> 27  
caagacagaaa agcttggttc cacttgcaaa atacaatttt tcatcataacc cctcgctgct 60  
ggcacagaaa tacacagcag agtcactgtt caggagtcga catgaagtta atgagcttgt 120  
cagtgtctca ggtgagaaac gacctggaac tgattcattt agattgagtc cctgattaaa 180  
gtagataaac atgatcttca gcagttgctt gaggtcttgc ttataccagt acatagcatt 240  
atggcccaga ttttgtcac attttagtaa cttcttcgat cccacgtgcg cgatgaggta 300  
tcttgagtc tgggaaactg ttgtgtccag ggggtgctgct cccaggaggc agaggaccat 360  
acagcagagg aacccggagc ccatggtgga gacaggcaca gtctggtcct cagtgtctcg 420  
gcc 423

<210> 28  
<211> 333  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (1)..(333)

<400> 28  
atc gga ctc ctc tgt ggt gtg gcc ttt tgt ttc ctg gga gta ggc ctt 48  
Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu  
1 5 10 15  
ttg aac gca caa gtg act caa acc ccg aga caa ctc atc aaa aaa gtg 96  
Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val  
20 25 30  
gga gcg aaa gtt ttg ttg aaa tgt tca cag aat atg gac cat gaa aga 144  
Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg  
35 40 45  
atg ttc tgg tat cga caa gac cca ggt ctg ggg ttg cgg ctg ctc tac 192  
Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr  
50 55 60  
tgg tcc tat aat att gac agt gtt gag aca gga gac atc cct tat ggg 240  
Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly  
65 70 75 80  
tac agt gtc tcg agg aag aag aag gat gcc ttc ccc ttg att ctg gag 288  
Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu  
85 90 95  
tct gct cgc atc aac cag aca tct gtg tac ttc tgc gcc agc agc 333  
Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser  
100 105 110

<210> 29  
 <211> 111  
 <212> PRT  
 <213> Canis familiaris  
 <400> 29  
 Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu  
     1                    5                    10                    15  
 Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val  
                     20                    25                    30  
 Gly Ala Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg  
                     35                    40                    45  
 Met Phe Trp Tyr Arg Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr  
                     50                    55                    60  
 Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly  
                     65                    70                    75                    80  
 Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu  
                     85                    90                    95  
 Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser  
                     100                    105                    110

<210> 30  
 <211> 333  
 <212> DNA  
 <213> Canis familiaris  
 <400> 30  
 gctactggcg cagaagtaca cagatgtctg gttgatgcga gcagactcca gaatcaaggg 60  
 gaaggcatcc ttcttcttcc tcgagacact gtaccataa gggatgtctc ctgtctcaac 120  
 actgtcaata ttataggacc agtagagcag ccgcaacccc agacctgggt cttgtcgata 180  
 ccagaacatt ctttcatggt ccatattctg tgaacatttc aacaaaactt tcgctccac 240  
 ttttttgatg agttgtctcg gggtttgagt cacttgtgcg ttcaaaaggc ctactcccag 300  
 gaaacaaaag gccacaccac agaggagtcc gat 333

<210> 31  
 <211> 351  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (25)..(351)

<400> 31  
 acggtgaagg gctagcacct aaag atg ctg act tgc ctg cta ctc ctc ctg 51

Met Leu Thr Cys Leu Leu Leu Leu Leu  
1 5

gga caa ggc tct gtg ttt gga gct ctt gtc tct caa aag ccg cgc agg 99  
Gly Gln Gly Ser Val Phe Gly Ala Leu Val Ser Gln Lys Pro Arg Arg  
10 15 20 25

gac atc tgt caa cgt ggg acc tcc att acc atc cac tgt gag gtc gat 147  
Asp Ile Cys Gln Arg Gly Thr Ser Ile Thr Ile His Cys Glu Val Asp  
30 35 40

acc caa gtc acc ttg atg ttc tgg tac cgt cag ctc cca gga cag agc 195  
Thr Gln Val Thr Leu Met Phe Trp Tyr Arg Gln Leu Pro Gly Gln Ser  
45 50 55

ttg ata ctg att gca acc gca aac cag ggt gca gag gcc acc tac gaa 243  
Leu Ile Leu Ile Ala Thr Ala Asn Gln Gly Ala Glu Ala Thr Tyr Glu  
60 65 70

agt gga ttt acc agg gag aag ttt ccc atc agc cgc cga acc cta atg 291  
Ser Gly Phe Thr Arg Glu Lys Phe Pro Ile Ser Arg Arg Thr Leu Met  
75 80 85

ttc tcc act ctg act gtg agc aac ctg agc ctc gaa gac acc agc tct 339  
Phe Ser Thr Leu Thr Val Ser Asn Leu Ser Leu Glu Asp Thr Ser Ser  
90 95 100 105

tac ttc tgc agc 351  
Tyr Phe Cys Ser

<210> 32  
<211> 109  
<212> PRT  
<213> Canis familiaris

<400> 32  
Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly  
1 5 10 15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr  
20 25 30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe  
35 40 45

Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala  
50 55 60

Asn Gln Gly Ala Glu Ala Thr Tyr Glu Ser Gly Phe Thr Arg Glu Lys  
65 70 75 80

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser  
85 90 95

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Ser

<210> 33  
 <211> 351  
 <212> DNA  
 <213> Canis familiaris

<400> 33  
 gctgcagaag taagagctgg tgtcttcgag gctcagggtg ctcacagtca gagtggagaa 60  
 cattaggggtt cggcggctga tgggaaactt ctccctggta aatccacttt cgtagggtggc 120  
 ctctgcaccc tggtttgccg ttgcaatcag tatcaagctc tgtcctggga gctgacggta 180  
 ccagaacatc aagggtgactt gggatatcgac ctcacagtgg atggtaatgg aggtcccacg 240  
 ttgacagatg tccctgcgcg gcttttgaga gacaagagct ccaaacacag agccttgtcc 300  
 caggaggagt agcaggcaag tcagcatctt taggtgctag cccttcaccg t 351

<210> 34  
 <211> 339  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (7)..(339)

<400> 34  
 gctgaa atg gcc acc ggc gtc ttc ttt ggc atg gct ctt tgt gtc ctg 48  
 Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu  
 1 5 10  
 tgg aca gga tac atg gat gct gga att atc cag agc cca aga tac aag 96  
 Trp Thr Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys  
 15 20 25 30  
 gtc aca ggg aca gga aag agg gtg act ctg aga tgt cac cag aca gac 144  
 Val Thr Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp  
 35 40 45  
 aac tat gac tat atg tac tgg tat cga cat gac ctg gga cat ggg ccg 192  
 Asn Tyr Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro  
 50 55 60  
 agg ctg atc tat tat tca aat ggt att aac agc act gaa aaa gga gac 240  
 Arg Leu Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp  
 65 70 75  
 ctc tcc aat gga tac aca gtc tct aga tca aac aag atg gat ttc ccc 288  
 Leu Ser Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro  
 80 85 90  
 ctc cta ctg gac tct gtt acc tcc tcc cag aca tct gtg tac ttc tgt 336  
 Leu Leu Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys

95 100 105 110 339  
gcc  
Ala

<210> 35  
<211> 111  
<212> PRT  
<213> Canis familiaris

<400> 35  
Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr  
1 5 10 15

Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr  
20 25 30

Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr  
35 40 45

Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu  
50 55 60

Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser  
65 70 75 80

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu  
85 90 95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Ala  
100 105 110

<210> 36  
<211> 339  
<212> DNA  
<213> Canis familiaris

<400> 36  
ggcacagaag tacacagatg tctgggagga ggtaacagag tccagtagga gggggaaatc 60  
catcttgttt gatctagaga ctgtgtatcc attggagagg tctccttttt cagtgtgttt 120  
aataccattt gaataataga tcagcctcgg cccatgtccc aggtcatgtc gataccagta 180  
catatagtca tagttgtctg tctggtgaca tctcagagtc accctctttc ctgtccctgt 240  
gaccttgat cttgggctct ggataattcc agcatccatg tatcctgtcc acaggacaca 300  
aagagccatg ccaaagaaga cgccggtggc catttcagc 339

<210> 37  
<211> 423  
<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (85)..(423)

<400> 37

aattaaccct cactaaaggg aacaaaaagct ggagctccac cgcggcacga ggagcgggga 60

ggctatcagc ttcccagggc tgcc atg ggc tcc agg ctt ctc tgc tgt gtg 111  
Met Gly Ser Arg Leu Leu Cys Cys Val  
1 5

gcc ctt tgt ctc ctg gga gcc ggc ccc gtg gag tct gag gtc atc caa 159  
Ala Leu Cys Leu Leu Gly Ala Gly Pro Val Glu Ser Glu Val Ile Gln  
10 15 20 25

act cca aga cac atg atc aaa gca aga gga cag aca gtg acc ctg aga 207  
Thr Pro Arg His Met Ile Lys Ala Arg Gly Gln Thr Val Thr Leu Arg  
30 35 40

tgt tcc ctt atc tct gga cac cta tct gtg tac tgg tac caa cag gcc 255  
Cys Ser Leu Ile Ser Gly His Leu Ser Val Tyr Trp Tyr Gln Gln Ala  
45 50 55

ctg ggc cag ggt ccc cgg ttt ctc att cag tat tac aat agg gaa gag 303  
Leu Gly Gln Gly Pro Arg Phe Leu Ile Gln Tyr Tyr Asn Arg Glu Glu  
60 65 70

aga gac aaa gga gac atc ccg gca aga ttc tca gtg cag cag ttc agt 351  
Arg Asp Lys Gly Asp Ile Pro Ala Arg Phe Ser Val Gln Gln Phe Ser  
75 80 85

aac tac agc tcc cag ctg gag atg aac tcc ctg gag cca gga gac tca 399  
Asn Tyr Ser Ser Gln Leu Glu Met Asn Ser Leu Glu Pro Gly Asp Ser  
90 95 100 105

gcc cta tat ctc tgt gcc agc agc 423  
Ala Leu Tyr Leu Cys Ala Ser Ser  
110

<210> 38

<211> 113

<212> PRT

<213> Canis familiaris

<400> 38

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala  
1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys  
20 25 30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His  
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe  
50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro  
 65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu  
 85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser  
 100 105 110

Ser

<210> 39  
 <211> 423  
 <212> DNA  
 <213> Canis familiaris

<400> 39  
 gctgctggca cagagatata gggctgagtc tcttggtccc agggagtcca tctccagctg 60  
 ggagctgtag ttactgaact gctgcactga gaatcttgcc gggatgtctc ctttgtctct 120  
 ctcttcccta ttgtaatact gaatgagaaa ccgggggaccc tggcccaggc cctgttggtg 180  
 ccagtaacaca gataggtgtc cagagataag ggaacatctc agggtcactg tctgtcctct 240  
 tgctttgatc atgtgtcttg gagtttggat gacctcagac tccacggggc cggctcccag 300  
 gagacaaagg gccacacagc agagaagcct ggagcccatg gcagccctgg gaagctgata 360  
 gcctcccgc tctcgtgcc gcggtggagc tccagctttt gttcccttta gtgagggtta 420  
 att 423

<210> 40  
 <211> 396  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (73)..(396)

<400> 40  
 gctgcaggat tcggcacgag gcgtgggtcat atctatcttg agagaggtat ggtatgaggc 60  
 catcacctga ag atg ctg atg ctt ctg ctg ctc ctg ggg ccc agc tct gga 111  
 Met Leu Met Leu Leu Leu Leu Leu Gly Pro Ser Ser Gly  
 1 5 10  
 ctc ggt gcc ctc gtc ttc cag gcg ccc agc aca atg atc tgt aag agc 159  
 Leu Gly Ala Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser  
 15 20 25

gga gcc acc gtg cag atc cag tgt caa aca gtg gac ctt caa gcc aca	207
Gly Ala Thr Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr	
30 35 40 45	
acc gtg ttt tgg tat cgc cag ctc ccg aag cag ggc ctt acc ctt atg	255
Thr Val Phe Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met	
50 55 60	
gtg acc tct aac gtg ggc aac agt gct aca cac gag cag ggg ttc cct	303
Val Thr Ser Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro	
65 70 75	
gca gcc aag ttc cct gtt aac cac cca aac ctc acg ttt tcc tcc ctg	351
Ala Ala Lys Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu	
80 85 90	
atg gtg acg agt tca ggt cct gga gac agc ggc ctc tac ttc tgt	396
Met Val Thr Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys	
95 100 105	

<210> 41  
 <211> 108  
 <212> PRT  
 <213> Canis familiaris

<400> 41	
Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala	
1 5 10 15	
Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr	
20 25 30	
Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe	
35 40 45	
Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser	
50 55 60	
Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys	
65 70 75 80	
Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr	
85 90 95	
Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys	
100 105	

<210> 42  
 <211> 396  
 <212> DNA  
 <213> Canis familiaris

<400> 42  
 acagaagtag aggccgctgt ctccaggacc tgaactcgtc accatcaggg agggaaaacgt 60



gaggtttggg tggttaacag ggaacttggc tgcagggaaac ccctgctcgt gtgtagcact 120  
 gttgcccacg ttagagggtca ccataaggggt aaggccctgc ttcgggagct ggcgatacca 180  
 aaacacgggtt gtggcttgaa ggtccactgt ttgacactgg atctgcacgg tggctccgct 240  
 cttacagatc attgtgctgg gcgcctggaa gacgagggca ccgagtccag agctggggccc 300  
 caggagcagc agaagcatca gcattctcag gtgatggcct cataccatac ctctctcaag 360  
 atagatatga ccacgcctcg tgccgaatcc tgcagc 396

<210> 43  
 <211> 354  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (13)..(354)

<400> 43  
 cacgagcctg cc atg tgc cca gtg ttc atc tgc tcc ttg gtc ctc tgg ctc 51  
                   Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu  
                   1                  5                  10  
  
 ctg agt aca ggc acc ctc aat gca aaa gtc atg cag act cca gga cat 99  
 Leu Ser Thr Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His  
           15                  20                  25  
 ctg gtc aaa ggg aaa gga caa aaa gca aaa atg gaa tgt gtc cca ata 147  
 Leu Val Lys Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile  
           30                  35                  40                  45  
  
 aaa gga cat agt tat gtt ttc tgg tat cag cag atc cca gca aaa gag 195  
 Lys Gly His Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu  
                   50                  55                  60  
  
 ttc aag ttc ttg att tct ttc cag gat aac gct gtc ttt gat aaa aca 243  
 Phe Lys Phe Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr  
                   65                  70                  75  
  
 ggg atg ccc acg cag aga ttt tta gcc ttg tgt cca aaa aac cta ccc 291  
 Gly Met Pro Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro  
           80                  85                  90  
  
 tgt agc cta gag atc gag cgt aca gag ctg cag gat tca gcc gtg tat 339  
 Cys Ser Leu Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr  
           95                  100                  105  
  
 ttt tgt gcc agc agt 354  
 Phe Cys Ala Ser Ser  
 110

<210> 44  
 <211> 114

<212> PRT

<213> Canis familiaris

<400> 44

Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu Leu Ser Thr  
1 5 10 15

Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His Leu Val Lys  
20 25 30

Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile Lys Gly His  
35 40 45

Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe  
50 55 60

Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro  
65 70 75 80

Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu  
85 90 95

Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Ala  
100 105 110

Ser Ser

<210> 45

<211> 354

<212> DNA

<213> Canis familiaris

<400> 45

actgctggca caaaaataca cggctgaatc ctgcagctct gtacgctcga tctctaggct 60  
acagggtagg ttttttggac acaaggctaa aaatctctgc gtgggcatcc ctgttttata 120  
aaagacagcg ttatcctgga aagaaatcaa gaacttgaac tcttttgctg ggatctgctg 180  
ataccagaaa acataactat gtccttttat tgggacacat tccatttttg ctttttgtcc 240  
tttccctttg accagatgtc ctggagtctg catgactttt gcattgaggg tgccctgtact 300  
caggagccag aggaccaagg agcagatgaa cactgggcac atggcaggct cgtg 354

<210> 46

<211> 369

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (40)..(369)

<400> 46  
ggcacgagca ctgaggacca gactgtgcct gtctccacc atg ggc tcc ggg ttc 54  
Met Gly Ser Gly Phe  
1 5

ctc tgc tgt atg gtc ctc tgc ctc ctg gga gca gca ccc ctg gac aca 102  
Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala Ala Pro Leu Asp Thr  
10 15 20

aca gtt tcc cag act cca aga tac ctc atc gcg cac gtg gga tcg aag 150  
Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala His Val Gly Ser Lys  
25 30 35

aag tta cta aaa tgt gag caa aat ctg ggc cat aat gct atg tac tgg 198  
Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His Asn Ala Met Tyr Trp  
40 45 50

tat aag caa gac ctc aag caa ctg ctg aag atc atg ttt atc tac ttt 246  
Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile Met Phe Ile Tyr Phe  
55 60 65

aat cag gga ctc aat cta aat gaa tca gtt cca ggt cgt ttc tca cct 294  
Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro Gly Arg Phe Ser Pro  
70 75 80 85

gag aca ctg aca agc tca tta act tca tgt cga ctc ctg aac agt gac 342  
Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg Leu Leu Asn Ser Asp  
90 95 100

tct gct gtg tat ttc tgt gcc agc agc 369  
Ser Ala Val Tyr Phe Cys Ala Ser Ser  
105 110

<210> 47

<211> 110

<212> PRT

<213> Canis familiaris

<400> 47

Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala  
1 5 10 15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala  
20 25 30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His  
35 40 45

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile  
50 55 60

Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro  
65 70 75 80

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg  
85 90 95

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser  
 100 105 110

<210> 48  
 <211> 369  
 <212> DNA  
 <213> Canis familiaris

<400> 48  
 gctgctggca cagaaatata cagcagagtc actgttcagg agtcgacatg aagttaatga 60  
 gcttgctcagt gtctcaggtg agaaacgacc tggaactgat tcatttagat tgagtccctg 120  
 attaaagtag ataaacatga tcttcagcag ttgcttgagg tcttgcttat accagtacat 180  
 agcattatgg ccagatattt gctcacattt tagtaacttc ttogatccca cgtgcgcgat 240  
 gaggtatctt ggagtctggg aaactgttgt gtccaggggt gctgctccca ggaggcagag 300  
 gaccatacag cagaggaacc cggagcccat ggtggagaca ggcacagtct ggtcctcagt 360  
 gctcgtgcc 369

<210> 49  
 <211> 504  
 <212> DNA  
 <213> Canis familiaris

<400> 49  
 gaggatctgc agaaggtcac cctcccaag gtcacagtgt ttgaaccatc ggaagcagag 60  
 atctcgcgga ccagaaggc cactctcgtg tgcttgcca cgggcttcta ccccgaccac 120  
 gtggagctga gctgggtggg gaacgggaag gaggtcacga gtgggttcag caccgacccg 180  
 cagccctaca aggagaggcc cagcgagaat gactccagct actgtctgag cagccggctg 240  
 agggctctctg cctccttctg gcacaacccg cgcaaccact tccgctgcca agtccagttc 300  
 tatgggctcg gggacgacga tgagtggaaa tacgatagag tcaaaccat caccagaac 360  
 atcagtgctg aggcctgggg cagagcagac tgtggcttca cctcgggtgtc ctaccatcag 420  
 ggcgtcctgt ctgccaccat cctctatgag atcctgctgg gcaaggccac gctgtatgct 480  
 gtgctggtca gcatcctggg gctg 504

<210> 50  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
 <220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 50  
cgacaagacc caggtctgg 19

<210> 51  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 51  
gtcagctccc aggacagag 19

<210> 52  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 52  
catgacctgg gacatgggc 19

<210> 53  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 53  
gagatgttcc cttatctctg g 21

<210> 54  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 54  
cctctaacgt gggcaacag 19

<210> 55  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 55  
tcagcagatc ccagcaaaag 20

<210> 56  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 56  
agcaagacct caagcaactg 20

<210> 57  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 57  
gtgaccttct gcagatcctc 20

<210> 58  
<211> 19  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 58  
agctcagctc cacgtggtc 19

<210> 59  
<211> 19  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 59

tgctgaaccc actcgtgac

19

<210> 60

<211> 109

<212> PRT

<213> Canis familiaris

<220>

<223> At location 109, Xaa = Ala or Ser

<400> 60

Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu  
1 5 10 15

Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val  
20 25 30

Gly Arg Lys Val Leu Leu Lys Cys Ser Gln Asn Met Asp His Glu Arg  
35 40 45

Trp Ser Tyr Asn Ile Asp Ser Val Glu Thr Gly Asp Ile Pro Tyr Gly  
50 55 60

Met Phe Trp Tyr Gln Gln Asp Pro Gly Leu Gly Leu Arg Leu Leu Tyr  
65 70 75 80

Tyr Ser Val Ser Arg Lys Lys Lys Asp Ala Phe Pro Leu Ile Leu Glu  
85 90 95

Ser Ala Arg Ile Asn Gln Thr Ser Val Tyr Phe Cys Xaa  
100 105

<210> 61

<211> 110

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 109 and 110, Xaa =Ala or Ser

<400> 61

Ile Gly Leu Leu Cys Gly Val Ala Phe Cys Phe Leu Gly Val Gly Leu  
1 5 10 15

Leu Asn Ala Gln Val Thr Gln Thr Pro Arg Gln Leu Ile Lys Lys Val  
20 25 30

Gly	Arg	Lys	Val	Leu	Leu	Lys	Cys	Ser	Gln	Asn	Met	Asp	His	Glu	Arg
		35					40					45			
Trp	Ser	Tyr	Asn	Ile	Asp	Ser	Val	Glu	Thr	Gly	Asp	Ile	Pro	Tyr	Gly
		50				55					60				
Met	Phe	Trp	Tyr	Gln	Gln	Asp	Pro	Gly	Leu	Gly	Leu	Arg	Leu	Leu	Tyr
	65				70					75					80
Tyr	Ser	Val	Ser	Arg	Lys	Lys	Lys	Asp	Ala	Phe	Pro	Leu	Ile	Leu	Glu
				85					90					95	
Ser	Ala	Arg	Ile	Asn	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Xaa	Xaa		
			100					105					110		

<210> 62  
 <211> 111  
 <212> PRT  
 <213> Canis familiaris

<220>  
 <223> At locations 109, 110 and 111, Xaa= Ala or Ser

Ile	Gly	Leu	Leu	Cys	Gly	Val	Ala	Phe	Cys	Phe	Leu	Gly	Val	Gly	Leu
	1			5					10					15	
Leu	Asn	Ala	Gln	Val	Thr	Gln	Thr	Pro	Arg	Gln	Leu	Ile	Lys	Lys	Val
			20					25					30		
Gly	Arg	Lys	Val	Leu	Leu	Lys	Cys	Ser	Gln	Asn	Met	Asp	His	Glu	Arg
		35					40					45			
Trp	Ser	Tyr	Asn	Ile	Asp	Ser	Val	Glu	Thr	Gly	Asp	Ile	Pro	Tyr	Gly
		50				55					60				
Met	Phe	Trp	Tyr	Gln	Gln	Asp	Pro	Gly	Leu	Gly	Leu	Arg	Leu	Leu	Tyr
	65				70					75					80
Tyr	Ser	Val	Ser	Arg	Lys	Lys	Lys	Asp	Ala	Phe	Pro	Leu	Ile	Leu	Glu
				85					90					95	
Ser	Ala	Arg	Ile	Asn	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Xaa	Xaa	Xaa	
			100					105					110		

<210> 63  
 <211> 109  
 <212> PRT  
 <213> Canis familiaris

<220>  
 <223> At location 109, Xaa =Ala or Ser

Met	Leu	Thr	Cys	Leu	Leu	Leu	Leu	Leu	Gly	Gln	Gly	Ser	Val	Phe	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



1		5		10		15									
Ala	Leu	Val	Ser	Gln	Lys	Pro	Arg	Arg	Asp	Ile	Cys	Gln	Arg	Gly	Thr
		20						25					30		
Ser	Ile	Thr	Ile	His	Cys	Glu	Val	Asp	Thr	Gln	Val	Thr	Leu	Met	Phe
		35						40				45			
Trp	Tyr	Arg	Gln	Leu	Pro	Gly	Gln	Ser	Leu	Ile	Leu	Ile	Ala	Thr	Ala
	50					55					60				
Ala	Glu	Ala	Thr	Tyr	Glu	Asn	Gln	Gly	Ser	Gly	Phe	Thr	Arg	Glu	Lys
	65					70				75					80
Phe	Pro	Ile	Ser	Arg	Arg	Thr	Leu	Met	Phe	Ser	Thr	Leu	Thr	Val	Ser
				85					90					95	
Asn	Leu	Ser	Leu	Glu	Asp	Thr	Ser	Ser	Tyr	Phe	Cys	Xaa			
			100					105							

<210> 64  
 <211> 110  
 <212> PRT  
 <213> Canis familiaris

<220>  
 <223> At locations 109 and 110, Xaa = Ala or Ser

<400> 64
Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly
1 5 10 15
Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr
20 25 30
Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe
35 40 45
Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala
50 55 60
Ala Glu Ala Thr Tyr Glu Asn Gln Gly Ser Gly Phe Thr Arg Glu Lys
65 70 75 80
Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser
85 90 95
Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Xaa Xaa
100 105 110

<210> 65  
 <211> 111  
 <212> PRT  
 <213> Canis familiaris

<220>

<223> At locations 109, 110 and 111, Xaa =Ala or Ser

<400> 65

Met Leu Thr Cys Leu Leu Leu Leu Leu Gly Gln Gly Ser Val Phe Gly  
1 5 10 15

Ala Leu Val Ser Gln Lys Pro Arg Arg Asp Ile Cys Gln Arg Gly Thr  
20 25 30

Ser Ile Thr Ile His Cys Glu Val Asp Thr Gln Val Thr Leu Met Phe  
35 40 45

Trp Tyr Arg Gln Leu Pro Gly Gln Ser Leu Ile Leu Ile Ala Thr Ala  
50 55 60

Ala Glu Ala Thr Tyr Glu Asn Gln Gly Ser Gly Phe Thr Arg Glu Lys  
65 70 75 80

Phe Pro Ile Ser Arg Arg Thr Leu Met Phe Ser Thr Leu Thr Val Ser  
85 90 95

Asn Leu Ser Leu Glu Asp Thr Ser Ser Tyr Phe Cys Xaa Xaa Xaa  
100 105 110

<210> 66

<211> 111

<212> PRT

<213> Canis familiaris

<220>

<223> At location 111, Xaa = Ala or Ser

<400> 66

Met Ala Thr Gly Val Phe Phe Gly Met Ala Leu Cys Val Leu Trp Thr  
1 5 10 15

Gly Tyr Met Asp Ala Gly Ile Ile Gln Ser Pro Arg Tyr Lys Val Thr  
20 25 30

Gly Thr Gly Lys Arg Val Thr Leu Arg Cys His Gln Thr Asp Asn Tyr  
35 40 45

Asp Tyr Met Tyr Trp Tyr Arg His Asp Leu Gly His Gly Pro Arg Leu  
50 55 60

Ile Tyr Tyr Ser Asn Gly Ile Asn Ser Thr Glu Lys Gly Asp Leu Ser  
65 70 75 80

Asn Gly Tyr Thr Val Ser Arg Ser Asn Lys Met Asp Phe Pro Leu Leu  
85 90 95

Leu Asp Ser Val Thr Ser Ser Gln Thr Ser Val Tyr Phe Cys Xaa  
100 105 110

<210> 67

<211> 112

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 111 and 112, Xaa = Ala or Ser

<400> 67

Met	Ala	Thr	Gly	Val	Phe	Phe	Gly	Met	Ala	Leu	Cys	Val	Leu	Trp	Thr
1				5					10					15	
Gly	Tyr	Met	Asp	Ala	Gly	Ile	Ile	Gln	Ser	Pro	Arg	Tyr	Lys	Val	Thr
			20					25					30		

Gly	Thr	Gly	Lys	Arg	Val	Thr	Leu	Arg	Cys	His	Gln	Thr	Asp	Asn	Tyr
		35					40					45			

Asp	Tyr	Met	Tyr	Trp	Tyr	Arg	His	Asp	Leu	Gly	His	Gly	Pro	Arg	Leu
	50					55					60				

Ile	Tyr	Tyr	Ser	Asn	Gly	Ile	Asn	Ser	Thr	Glu	Lys	Gly	Asp	Leu	Ser
65					70					75				80	

Asn	Gly	Tyr	Thr	Val	Ser	Arg	Ser	Asn	Lys	Met	Asp	Phe	Pro	Leu	Leu
				85					90					95	

Leu	Asp	Ser	Val	Thr	Ser	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Xaa	Xaa
		100						105					110		

<210> 68

<211> 113

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 111, 112 and 113, Xaa = Ala or Ser

<400> 68

Met	Ala	Thr	Gly	Val	Phe	Phe	Gly	Met	Ala	Leu	Cys	Val	Leu	Trp	Thr
1				5					10					15	

Gly	Tyr	Met	Asp	Ala	Gly	Ile	Ile	Gln	Ser	Pro	Arg	Tyr	Lys	Val	Thr
			20					25					30		

Gly	Thr	Gly	Lys	Arg	Val	Thr	Leu	Arg	Cys	His	Gln	Thr	Asp	Asn	Tyr
		35					40					45			

Asp	Tyr	Met	Tyr	Trp	Tyr	Arg	His	Asp	Leu	Gly	His	Gly	Pro	Arg	Leu
	50					55					60				

Ile	Tyr	Tyr	Ser	Asn	Gly	Ile	Asn	Ser	Thr	Glu	Lys	Gly	Asp	Leu	Ser
65					70					75				80	

Asn	Gly	Tyr	Thr	Val	Ser	Arg	Ser	Asn	Lys	Met	Asp	Phe	Pro	Leu	Leu
				85					90					95	

Leu	Asp	Ser	Val	Thr	Ser	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Xaa	Xaa
		100						105					110		

Xaa

<210> 69  
<211> 111  
<212> PRT  
<213> Canis familiaris

<220>  
<223> At location 111, Xaa = Ala or Ser

<400> 69  
Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala  
1 5 10 15  
Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys  
20 25 30  
Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His  
35 40 45  
Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe  
50 55 60  
Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro  
65 70 75 80  
Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu  
85 90 95  
Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Xaa  
100 105 110

<210> 70  
<211> 112  
<212> PRT  
<213> Canis familiaris

<220>  
<223> At locations 111 and 112, Xaa = Ala or Ser

<400> 70  
Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala  
1 5 10 15  
Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys  
20 25 30  
Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His  
35 40 45  
Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe  
50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro  
65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu  
85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Xaa Xaa  
100 105 110

<210> 71

<211> 113

<212> PRT

<213> Canis familiaris

<220>

<223> At locations 111, 112 and 113, Xaa = Ala or Ser

<400> 71

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala  
1 5 10 15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys  
20 25 30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His  
35 40 45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe  
50 55 60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro  
65 70 75 80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu  
85 90 95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Xaa Xaa  
100 105 110

Xaa

<210> 72

<211> 109

<212> PRT

<213> Canis familiaris

<220>

<223> At location 109, Xaa = Ala or Ser

<400> 72

Met Leu Met Leu Leu Leu Leu Gly Pro Ser Ser Gly Leu Gly Ala  
1 5 10 15

Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr  
20 25 30

Val	Gln	Ile	Gln	Cys	Gln	Thr	Val	Asp	Leu	Gln	Ala	Thr	Thr	Val	Phe
			35					40					45		
Trp	Tyr	Arg	Gln	Leu	Pro	Lys	Gln	Gly	Leu	Thr	Leu	Met	Val	Thr	Ser
		50				55					60				
Asn	Val	Gly	Asn	Ser	Ala	Thr	His	Glu	Gln	Gly	Phe	Pro	Ala	Ala	Lys
	65				70					75					80
Phe	Pro	Val	Asn	His	Pro	Asn	Leu	Thr	Phe	Ser	Ser	Leu	Met	Val	Thr
				85					90					95	
Ser	Ser	Gly	Pro	Gly	Asp	Ser	Gly	Leu	Tyr	Phe	Cys	Xaa			
			100					105							

<210> 73  
 <211> 110  
 <212> PRT  
 <213> Canis familiaris

<220>  
 <223> At location 109 and 110, Xaa = Ala or Ser

Met	Leu	Met	Leu	Leu	Leu	Leu	Gly	Pro	Ser	Ser	Gly	Leu	Gly	Ala	
1				5				10					15		
Leu	Val	Phe	Gln	Ala	Pro	Ser	Thr	Met	Ile	Cys	Lys	Ser	Gly	Ala	Thr
			20					25					30		
Val	Gln	Ile	Gln	Cys	Gln	Thr	Val	Asp	Leu	Gln	Ala	Thr	Thr	Val	Phe
			35					40					45		
Trp	Tyr	Arg	Gln	Leu	Pro	Lys	Gln	Gly	Leu	Thr	Leu	Met	Val	Thr	Ser
		50				55					60				
Asn	Val	Gly	Asn	Ser	Ala	Thr	His	Glu	Gln	Gly	Phe	Pro	Ala	Ala	Lys
	65				70					75					80
Phe	Pro	Val	Asn	His	Pro	Asn	Leu	Thr	Phe	Ser	Ser	Leu	Met	Val	Thr
				85					90					95	
Ser	Ser	Gly	Pro	Gly	Asp	Ser	Gly	Leu	Tyr	Phe	Cys	Xaa	Xaa		
			100					105					110		

<210> 74  
 <211> 111  
 <212> PRT  
 <213> Canis familiaris

<220>  
 <223> At locations 109, 110 and 111, Xaa = Ala or Ser

Met	Leu	Met	Leu	Leu	Leu	Leu	Gly	Pro	Ser	Ser	Gly	Leu	Gly	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1	5	10	15
Leu Val Phe Gln Ala Pro Ser Thr Met Ile Cys Lys Ser Gly Ala Thr	20	25	30
Val Gln Ile Gln Cys Gln Thr Val Asp Leu Gln Ala Thr Thr Val Phe	35	40	45
Trp Tyr Arg Gln Leu Pro Lys Gln Gly Leu Thr Leu Met Val Thr Ser	50	55	60
Asn Val Gly Asn Ser Ala Thr His Glu Gln Gly Phe Pro Ala Ala Lys	65	70	75
Phe Pro Val Asn His Pro Asn Leu Thr Phe Ser Ser Leu Met Val Thr	85	90	95
Ser Ser Gly Pro Gly Asp Ser Gly Leu Tyr Phe Cys Xaa Xaa Xaa	100	105	110

<210> 75  
 <211> 112  
 <212> PRT  
 <213> Canis familiaris  
 <220>  
 <223> At location 112, Xaa = Ala or Ser

<400> 75
Met Cys Pro Val Phe Ile Cys Ser Leu Val Leu Trp Leu Leu Ser Thr
1 5 10 15
Gly Thr Leu Asn Ala Lys Val Met Gln Thr Pro Gly His Leu Val Lys
20 25 30
Gly Lys Gly Gln Lys Ala Lys Met Glu Cys Val Pro Ile Lys Gly His
35 40 45
Ser Tyr Val Phe Trp Tyr Gln Gln Ile Pro Ala Lys Glu Phe Lys Phe
50 55 60
Leu Ile Ser Phe Gln Asp Asn Ala Val Phe Asp Lys Thr Gly Met Pro
65 70 75 80
Thr Gln Arg Phe Leu Ala Leu Cys Pro Lys Asn Leu Pro Cys Ser Leu
85 90 95
Glu Ile Glu Arg Thr Glu Leu Gln Asp Ser Ala Val Tyr Phe Cys Xaa
100 105 110

<210> 76  
 <211> 113  
 <212> PRT  
 <213> Canis familiaris  
 <220>

<223> At location 112 and 113, Xaa = Ala or Ser

<400> 76

Met	Cys	Pro	Val	Phe	Ile	Cys	Ser	Leu	Val	Leu	Trp	Leu	Leu	Ser	Thr
1				5					10					15	

Gly	Thr	Leu	Asn	Ala	Lys	Val	Met	Gln	Thr	Pro	Gly	His	Leu	Val	Lys
			20					25					30		

Gly	Lys	Gly	Gln	Lys	Ala	Lys	Met	Glu	Cys	Val	Pro	Ile	Lys	Gly	His
		35					40					45			

Ser	Tyr	Val	Phe	Trp	Tyr	Gln	Gln	Ile	Pro	Ala	Lys	Glu	Phe	Lys	Phe
	50					55					60				

Leu	Ile	Ser	Phe	Gln	Asp	Asn	Ala	Val	Phe	Asp	Lys	Thr	Gly	Met	Pro
65					70					75					80

Thr	Gln	Arg	Phe	Leu	Ala	Leu	Cys	Pro	Lys	Asn	Leu	Pro	Cys	Ser	Leu
				85					90					95	

Glu	Ile	Glu	Arg	Thr	Glu	Leu	Gln	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Xaa
			100					105					110		

Xaa

<210> 77

<211> 114

<212> PRT

<213> Canis familiaris

<220>

<223> At location 112, 113 and 114, Xaa = Ala or Ser

<400> 77

Met	Cys	Pro	Val	Phe	Ile	Cys	Ser	Leu	Val	Leu	Trp	Leu	Leu	Ser	Thr
1				5					10					15	

Gly	Thr	Leu	Asn	Ala	Lys	Val	Met	Gln	Thr	Pro	Gly	His	Leu	Val	Lys
			20					25					30		

Gly	Lys	Gly	Gln	Lys	Ala	Lys	Met	Glu	Cys	Val	Pro	Ile	Lys	Gly	His
		35					40					45			

Ser	Tyr	Val	Phe	Trp	Tyr	Gln	Gln	Ile	Pro	Ala	Lys	Glu	Phe	Lys	Phe
	50					55					60				

Leu	Ile	Ser	Phe	Gln	Asp	Asn	Ala	Val	Phe	Asp	Lys	Thr	Gly	Met	Pro
65					70					75					80

Thr	Gln	Arg	Phe	Leu	Ala	Leu	Cys	Pro	Lys	Asn	Leu	Pro	Cys	Ser	Leu
				85					90					95	

Glu	Ile	Glu	Arg	Thr	Glu	Leu	Gln	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Xaa
			100					105					110		



Xaa Xaa

<210> 78  
<211> 108  
<212> PRT  
<213> Canis familiaris

<220>  
<223> At location 108, Xaa = Ala or Ser

<400> 78  
Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala  
1 5 10 15  
Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala  
20 25 30  
His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His  
35 40 45  
Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile  
50 55 60  
Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro  
65 70 75 80  
Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg  
85 90 95  
Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Xaa  
100 105

<210> 79  
<211> 109  
<212> PRT  
<213> Canis familiaris

<220>  
<223> At locations 108 and 109, Xaa = Ala or Ser

<400> 79  
Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala  
1 5 10 15  
Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala  
20 25 30  
His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His  
35 40 45  
Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile  
50 55 60  
Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro

65		70		75		80									
Gly	Arg	Phe	Ser	Pro	Glu	Thr	Leu	Thr	Ser	Ser	Leu	Thr	Ser	Cys	Arg
				85					90					95	

Leu	Leu	Asn	Ser	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Xaa	Xaa
		100					105					

<210> 80  
 <211> 110  
 <212> PRT  
 <213> Canis familiaris

<220>  
 <223> At locations 108, 109 and 110, Xaa = Ala or Ser

<400> 80
Met Gly Ser Gly Phe Leu Cys Cys Met Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Ala Pro Leu Asp Thr Thr Val Ser Gln Thr Pro Arg Tyr Leu Ile Ala
20 25 30

His Val Gly Ser Lys Lys Leu Leu Lys Cys Glu Gln Asn Leu Gly His
35 40 45

Asn Ala Met Tyr Trp Tyr Lys Gln Asp Leu Lys Gln Leu Leu Lys Ile
50 55 60

Met Phe Ile Tyr Phe Asn Gln Gly Leu Asn Leu Asn Glu Ser Val Pro
65 70 75 80

Gly Arg Phe Ser Pro Glu Thr Leu Thr Ser Ser Leu Thr Ser Cys Arg
85 90 95

Leu Leu Asn Ser Asp Ser Ala Val Tyr Phe Cys Xaa Xaa Xaa
100 105 110

<210> 81  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<220>  
 <223> Y = T or C , R = G or A, N = A, C, G, or T

<400> 81  
 ccgaattctg gtaycrnca

<210> 82  
 <211> 18  
 <212> DNA

<213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer  
 <220>  
 <223> R = G or A  
 <400> 82  
 cggatccgcr cartarta 18

<210> 83  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer  
 <220>  
 <223> R = G or A  
 <400> 83  
 cggatccgcr caraarta 18

<210> 84  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer  
 <400> 84  
 ccagacctgg gtcttgctg 19

<210> 85  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer  
 <400> 85  
 ctctgtcctg ggagctga 18

<210> 86  
 <211> 21

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         Primer  
  
 <400> 86  
 ttgtttgatc tagagactgt g 21  
  
  
 <210> 87  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         Primer  
  
 <400> 87  
 atcggactcc tctgtggtgt 20  
  
  
 <210> 88  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         Primer  
  
 <400> 88  
 acggtgaagg gctagcacct 20  
  
  
 <210> 89  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         Primer  
  
 <400> 89  
 gctgaaatgg ccaccggcgt 20  
  
  
 <210> 90  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

Primer

<400> 90  
ctgttgccca cgtttagagg 19

<210> 91  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 91  
ttactgaact gctgcactg 19

<210> 92  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 92  
gctgcaggat tcggcacgag 20

<210> 93  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 93  
tacgactgtc agcttggtcc 20

<210> 94  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 94  
cttttgctgg gatctgctga 20

<210> 95  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 95  
cagttgctta ggtcttgct 19

<210> 96  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 96  
cacgagcctg ccatgtgccc 20

<210> 97  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 97  
ggcacgagca ctgaggacca 20

<210> 98  
<211> 438  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (40)..(438)

<400> 98  
cacgaggagc ggggaggcta tcagcttccc agggctgcc atg ggc tcc agg ctt 54  
Met Gly Ser Arg Leu  
1 5

ctc tgc tgt gtg gcc ctt tgt ctc ctg gga gcc ggc ccc gtg gag tct 102  
Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala Gly Pro Val Glu Ser  
10 15 20

gag gtc atc caa act cca aga cac atg atc aaa gca aga gga cag aca 150  
 Glu Val Ile Gln Thr Pro Arg His Met Ile Lys Ala Arg Gly Gln Thr  
                   25                                  30                                  35

gtg acc ctg aga tgt tcc ctt atc tct gga cac cta tct gtg tac tgg 198  
 Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His Leu Ser Val Tyr Trp  
                   40                                  45                                  50

tac caa cag gcc ctg ggc cag ggt ccc cgg ttt ctc att cag tat tac 246  
 Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe Leu Ile Gln Tyr Tyr  
                   55                                  60                                  65

aat agg gaa gag aga gac aaa gga gac atc ccg gca aga ttc tca gtg 294  
 Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro Ala Arg Phe Ser Val  
                   70                                  75                                  80                                  85

cag cag ttc agt aac tac agc tcc cag ctg gag atg aac tcc ctg gag 342  
 Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu Met Asn Ser Leu Glu  
                                   90                                  95                                  100

cca gga gac tca gcc cta tat ctc tgt gcc agc agc tta gat gcg ttc 390  
 Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Leu Asp Ala Phe  
                                   105                                  110                                  115

gac gcg ggg cag ctg tac ttc ggg gcc ggt tcc aag ctg gcc gtg ctg 438  
 Asp Ala Gly Gln Leu Tyr Phe Gly Ala Gly Ser Lys Leu Ala Val Leu  
                   120                                  125                                  130

<210> 99

<211> 133

<212> PRT

<213> Canis familiaris

<400> 99

Met Gly Ser Arg Leu Leu Cys Cys Val Ala Leu Cys Leu Leu Gly Ala  
                   1                                  5                                  10                                  15

Gly Pro Val Glu Ser Glu Val Ile Gln Thr Pro Arg His Met Ile Lys  
                                   20                                  25                                  30

Ala Arg Gly Gln Thr Val Thr Leu Arg Cys Ser Leu Ile Ser Gly His  
                   35                                  40                                  45

Leu Ser Val Tyr Trp Tyr Gln Gln Ala Leu Gly Gln Gly Pro Arg Phe  
                   50                                  55                                  60

Leu Ile Gln Tyr Tyr Asn Arg Glu Glu Arg Asp Lys Gly Asp Ile Pro  
                   65                                  70                                  75                                  80

Ala Arg Phe Ser Val Gln Gln Phe Ser Asn Tyr Ser Ser Gln Leu Glu  
                                   85                                  90                                  95

Met Asn Ser Leu Glu Pro Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser  
                   100                                  105                                  110

Ser Leu Asp Ala Phe Asp Ala Gly Gln Leu Tyr Phe Gly Ala Gly Ser  
115 120 125

Lys Leu Ala Val Leu  
130

<210> 100  
<211> 438  
<212> DNA  
<213> Canis familiaris

<400> 100  
cagcacggcc agcttggaac cggccccgaa gtacagctgc cccgcgtcga acgcatctaa 60  
gctgctggca cagagatata gggctgagtc tcttggtcc agggagtcca tctccagctg 120  
ggagctgtag ttactgaact gctgcactga gaatcttgcc gggatgtctc ctttgtctct 180  
ctcttccta ttgtaatact gaatgagaaa ccggggaccc tggcccaggg cctgttggtta 240  
ccagtacaca gataggtgtc cagagataag ggaacatctc agggtcactg tctgtcctct 300  
tgctttgatc atgtgtcttg gagtttggat gacctcagac tccacggggc cggctcccag 360  
gagacaaagg gccacacagc agagaagcct ggagcccatg gcagccctgg gaagctgata 420  
gcctccccgc tctcgtg 438